

RAW SEQUENCE LISTING

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Application Serial Number: 10/595,858
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RAW SEQUENCE LISTING

DATE: 06/02/2006

PATENT APPLICATION: US/10/595,858

TIME: 09:22:00

Input Set : A:\Sequence Listing to File.TXT

Output Set: N:\CRF4\06022006\J595858.raw

3 <110> APPLICANT: YOSHINAGA, Takashi
 4 ARAI, Toru
 6 <120> TITLE OF INVENTION: hERG channel-expressing cell
 8 <130> FILE REFERENCE: 09857/0204372-US0
 10 <140> CURRENT APPLICATION NUMBER: 10/595,858
 11 <141> CURRENT FILING DATE: 2006-05-16
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/017441
 14 <151> PRIOR FILING DATE: 2004-11-17
 16 <150> PRIOR APPLICATION NUMBER: JP 2003-387255
 17 <151> PRIOR FILING DATE: 2003-11-17
 19 <160> NUMBER OF SEQ ID NOS: 13
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 4070
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo Sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (184)..(3660)
 33 <400> SEQUENCE: 1

34	acgcggcctg ctcagggcctc cagcgccgg tcggagggga ggccgggaggc gagcgaggac	60
36	ccgcgcggc agtccagtct gtgcgcgccc gtgcgtcgctt ggccgggtgc gggaccagcg	120
38	ccggccaccc gaagccatgt gcgtcgccgg gtgggtgggc ccgcggcgcc ccatgggctc	180
40	agg atg ccg gtg cgg agg ggc cac gtc gcg ccg cag aac acc ttc ctg	228
41	Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu	
42	1 5 10 15	
44	gac acc atc atc cgc aag ttt gag ggc cag agc cgt aag ttc atc atc	276
45	Asp Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile	
46	20 25 30	
48	gcc aac gct cgg gtg gag aac tgc gcc gtc atc tac tgc aac gac ggc	324
49	Ala Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly	
50	35 40 45	
52	tgc tgc gag ctg tgc ggc tac tgc cgg gcc gag gtg atg cag cga ccc	372
53	Phe Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro	
54	50 55 60	
56	tgc acc tgc gac ttc ctg cac ggg ccc cgc acg cag cgc cgc gct gcc	420
57	Cys Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala	
58	65 70 75	
60	gct cag atc gct cag gca ctg ctg ggc gag gag cgc aaa gtg gaa	468
61	Ala Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu	
62	80 85 90 95	
64	atc gcc ttc tac cgg aaa gat ggg agc tgc ttc cta tgt ctg gtg gat	516
65	Ile Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp	

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66	100	105	110	
68	gtg gtg ccc gtg aag aac gag gat ggg gct gtc atc atg ttc atc ctc			564
69	Val Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu			
70	115	120	125	
72	aat ttc gag gtg atg gag aag gac atg gtg ggg tcc ccg gct cat			612
73	Asn Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His			
74	130	135	140	
76	gac acc aac cac cgg ggc ccc ccc acc agc tgg ctg gcc cca ggc cgc			660
77	Asp Thr Asn His Arg Gly Pro Pro Thr Ser Trp Leu Ala Pro Gly Arg			
78	145	150	155	
80	gcc aag acc ttc cgc ctg aag ctg ccc gcg ctg ctg gcg ctg acg gcc			708
81	Ala Lys Thr Phe Arg Leu Lys Leu Pro Ala Leu Leu Ala Leu Thr Ala			
82	160	165	170	175
84	cgg gag tcg tcg gtg cgg tcg ggc ggc ggc ggc ggc ggc ggc ccc			756
85	Arg Glu Ser Ser Val Arg Ser Gly Gly Ala Gly Gly Ala Pro			
86	180	185	190	
88	ggg gcc gtg gtg gac gtg gac ctg acg ccc gcg gca ccc agc agc			804
89	Gly Ala Val Val Asp Val Asp Leu Thr Pro Ala Ala Pro Ser Ser			
90	195	200	205	
92	gag tcg ctg gcc ctg gac gaa gtg aca gcc atg gac aac cac gtg gca			852
93	Glu Ser Leu Ala Leu Asp Glu Val Thr Ala Met Asp Asn His Val Ala			
94	210	215	220	
96	ggg ctc ggg ccc gcg gag gag cgg cgt gcg ctg gtg ggt ccc ggc tct			900
97	Gly Leu Gly Pro Ala Glu Glu Arg Arg Ala Leu Val Gly Pro Gly Ser			
98	225	230	235	
100	ccc ccc cgc agc gcg ccc ggc cag ctc cca tcg ccc cgg gcg cac agc			948
101	Pro Pro Arg Ser Ala Pro Gly Gln Leu Pro Ser Pro Arg Ala His Ser			
102	240	245	250	255
104	ctc aac ccc gac gcc tcg ggc tcc agc tgc agc ctg gcc cgg acg cgc			996
105	Leu Asn Pro Asp Ala Ser Gly Ser Ser Cys Ser Leu Ala Arg Thr Arg			
106	260	265	270	
108	tcc cga gaa agc tgc gcc agc gtg cgc cgc gcc tcg tcg gcc gac gac			1044
109	Ser Arg Glu Ser Cys Ala Ser Val Arg Arg Ala Ser Ser Ala Asp Asp			
110	275	280	285	
112	atc gag gcc atg cgc gcc ggg gtg ctg ccc cgg cca ccg cgc cac gcc			1092
113	Ile Glu Ala Met Arg Ala Gly Val Leu Pro Pro Pro Arg His Ala			
114	290	295	300	
116	agc acc ggg gcc atg cac cca ctg cgc agc ggc ttg ctc aac tcc acc			1140
117	Ser Thr Gly Ala Met His Pro Leu Arg Ser Gly Leu Leu Asn Ser Thr			
118	305	310	315	
120	tcg gac tcc gac ctc gtg cgc tac cgc acc att agc aag att ccc caa			1188
121	Ser Asp Ser Asp Leu Val Arg Tyr Arg Thr Ile Ser Lys Ile Pro Gln			
122	320	325	330	335
124	atc acc ctc aac ttt gtg gac ctc aag ggc gac ccc ttc ttg gct tcg			1236
125	Ile Thr Leu Asn Phe Val Asp Leu Lys Gly Asp Pro Phe Leu Ala Ser			
126	340	345	350	
128	ccc acc agt gac cgt gag atc ata gca cct aag ata aag gag cga acc			1284
129	Pro Thr Ser Asp Arg Glu Ile Ile Ala Pro Lys Ile Lys Glu Arg Thr			
130	355	360	365	

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132 cac aat gtc act gag aag gtc acc cag gtc ctg tcc ctg ggc gcc gac	1332
133 His Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp	
134 370 375 380	
136 gtg ctg cct gag tac aag ctg cag gca ccg cgc atc cac cgc tgg acc	1380
137 Val Leu Pro Glu Tyr Lys Leu Gln Ala Pro Arg Ile His Arg Trp Thr	
138 385 390 395	
140 atc ctg cat tac agc ccc ttc aag gcc gtg tgg gac tgg ctc atc ctg	1428
141 Ile Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu	
142 400 405 410 415	
144 ctg ctg gtc atc tac acg gct gtc ttc aca ccc tac tcg gct gcc ttc	1476
145 Leu Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe	
146 420 425 430	
148 ctg ctg aag gag acg gaa gaa ggc ccg cct gct acc gag tgt ggc tac	1524
149 Leu Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr	
150 435 440 445	
152 gcc tgc cag ccg ctg gct gtg gtg gac ctc atc gtg gac atc atg ttc	1572
153 Ala Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met Phe	
154 450 455 460	
156 att gtg gac atc ctc atc aac ttc ccg acc acc tac gtc aat gcc aac	1620
157 Ile Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala Asn	
158 465 470 475	
160 gag gag gtg gtc agc cac ccc ggc ccg atc gcc gtc cac tac ttc aag	1668
161 Glu Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe Lys	
162 480 485 490 495	
164 ggc tgg ttc ctc atc gac atg gtg gcc gcc atc ccc ttc gac ctg ctc	1716
165 Gly Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu	
166 500 505 510	
168 atc ttc ggc tct ggc tct gag gag ctg atc ggg ctg ctg aag act gcg	1764
169 Ile Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr Ala	
170 515 520 525	
172 cgg ctg ctg cgg ctg gtg ccg gtg gcg ccg aag ctg gat ccg tac tca	1812
173 Arg Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser	
174 530 535 540	
176 gag tac ggc gcg gcc gtg ctg ttc ttg ctc atg tgc acc ttt gcg ctc	1860
177 Glu Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala Leu	
178 545 550 555	
180 atc gcg cac tgg cta gcc tgc atc tgg tac gcc atc ggc aac atg gag	1908
181 Ile Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met Glu	
182 560 565 570 575	
184 cag cca cac atg gac tca ccg atc ggc tgg ctg cac aac ctg ggc gac	1956
185 Gln Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly Asp	
186 580 585 590	
188 cag ata ggc aaa ccc tac aac agc agc ggc ctg ggc ggc ccc tcc atc	2004
189 Gln Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser Ile	
190 595 600 605	
192 aag gac aag tat gtg acg gcg ctc tac ttc acc ttc agc agc ctc acc	2052
193 Lys Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr	
194 610 615 620	
196 agt gtg ggc ttc ggc aac gtc tct ccc aac acc aac tca gag aag atc	2100

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197 Ser Val Gly Phe Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Ile		
198 625 630 635		
200 ttc tcc atc tgc gtc atg ctc att ggc tcc ctc atg tat gct agc atc	2148	
201 Phe Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile		
202 640 645 650 655		
204 ttc ggc aac gtg tcg gcc atc atc cag cgg ctg tac tcg ggc aca gcc	2196	
205 Phe Gly Asn Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala		
206 660 665 670 675		
208 cgc tac cac aca cag atg ctg cgg gtg cgg gag ttc atc cgc ttc cac	2244	
209 Arg Tyr His Thr Gln Met Leu Arg Val Arg Glu Phe Ile Arg Phe His		
210 675 680 685		
212 cag atc ccc aat ccc ctg cgc cag cgc ctc gag gag tac ttc cag cac	2292	
213 Gln Ile Pro Asn Pro Leu Arg Gln Arg Leu Glu Tyr Phe Gln His		
214 690 695 700		
216 gcc tgg tcc tac acc aac ggc atc gac atg aac gcg gtg ctg aag ggc	2340	
217 Ala Trp Ser Tyr Thr Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly		
218 705 710 715		
220 ttc cct gag tgc ctg cag gct gac atc tgc ctg cac ctg aac cgc tca	2388	
221 Phe Pro Glu Cys Leu Gln Ala Asn Ile Cys Leu His Leu Asn Arg Ser		
222 720 725 730 735		
224 ctg ctg cag cac tgc aaa ccc ttc cga ggg gcc acc aag ggc tgc ctt	2436	
225 Leu Leu Gln His Cys Lys Pro Phe Arg Gly Ala Thr Lys Gly Cys Leu		
226 740 745 750		
228 cgg gcc ctg gcc atg aag ttc aag acc aca cat gca ccg cca ggg gac	2484	
229 Arg Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp		
230 755 760 765		
232 aca ctg gtg cat gct ggg gac ctg ctc acc gcc ctg tac ttc atc tcc	2532	
233 Thr Leu Val His Ala Gly Asp Leu Leu Thr Ala Leu Tyr Phe Ile Ser		
234 770 775 780		
236 cgg ggc tcc atc gag atc ctg cgg ggc gac gtc gtc gtg gcc atc ctg	2580	
237 Arg Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile Leu		
238 785 790 795		
240 ggg aag aat gac atc ttt ggg gag cct ctg aac ctg tat gca agg cct	2628	
241 Gly Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg Pro		
242 800 805 810 815		
244 ggc aag tcg aac ggg gat gtg cgg gcc ctc acc tac tgt gac cta cac	2676	
245 Gly Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His		
246 820 825 830		
248 aag atc cat cgg gac gac ctg ctg gag gtg ctg gac atg tac cct gag	2724	
249 Lys Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Glu		
250 835 840 845		
252 ttc tcc gac cac ttc tgg tcc agc ctg gag atc acc ttc aac ctg cga	2772	
253 Phe Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu Arg		
254 850 855 860		
256 gat acc aac atg atc ccg ggc tcc ccc ggc agt acg gag tta gag ggt	2820	
257 Asp Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu Gly		
258 865 870 875		
260 ggc ttc agt cgg caa cgc aag cgc aag ttg tcc ttc cgc agg cgc acg	2868	
261 Gly Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg Thr		

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262	880	885	890	895	
264	gac aag gac acg gag cag cca	ggg gag gtg tcg	gcc ttg	ggg ccg ggc	2916
265	Lys Asp Thr Glu Gln Pro Gly	Glu Val Ser Ala Leu Gly	Pro Gly		
266	900	905	910		
268	cgg gcg ggg gca	ggg ccg agt agc	cggttcc	ccg ggg ggg ccg tgg	2964
269	Arg Ala Gly Ala Gly	Pro Ser Ser Arg Gly	Arg Pro Gly	Gly Pro Trp	
270	915	920	925		
272	ggg gag agc ccg tcc	agt ggc ccc tcc	agc cct gag	agc agt gag gat	3012
273	Gly Glu Ser Pro Ser Ser Gly	Pro Ser Ser Pro Gly	Ser Ser Glu	Ser Glu Asp	
274	930	935	940		
276	gag ggc cca ggc cgc	agc tcc agc ccc	ctc cgc ctg	gtg ccc ttc tcc	3060
277	Glu Gly Pro Gly Arg Ser	Ser Ser Pro Leu Arg	Leu Val Pro Phe Ser		
278	945	950	955		
280	agc ccc agg ccc ccc gga	gag ccg ccg ggt	ggg gag ccc ctg	atg gag	3108
281	Ser Pro Arg Pro Pro Gly	Glu Pro Pro Gly	Gly Glu Pro	Leu Met Glu	
282	960	965	970	975	
284	gac tgc gag aag agc	agc gac act tgc	aac ccc ctg tca	ggc gcc ttc	3156
285	Asp Cys Glu Lys Ser Ser Asp	Thr Cys Asn Pro	Leu Ser Gly	Ala Phe	
286	980	985	990		
288	tca gga gtg tcc aac att	ttc agc ttc	tgg ggg gac	agt cgg ggc cgc	3204
289	Ser Gly Val Ser Asn Ile	Phe Ser Phe	Trp Gly Asp Ser Arg	Gly Arg	
290	995	1000	1005		
292	cag tac cag gag ctc	cct cga tgc	ccc gcc ccc acc	ccc agc ctc	3249
293	Gln Tyr Gln Glu Leu Pro Arg	Cys Pro Ala Pro	Thr Pro Ser	Leu	
294	1010	1015	1020		
296	ctc aac atc ccc ctc tcc	agc ccg	ggt cgg cgg ccc	ccg ggc gac	3294
297	Leu Asn Ile Pro Leu Ser Ser	Pro Pro Gly	Arg Arg Pro Arg	Gly Asp	
298	1025	1030	1035		
300	gtg gag agc agg ctg	gat gcc ctc	cag cgc cag ctc	aac agg ctg	3339
301	Val Glu Ser Arg Leu Asp	Ala Leu Gln Arg	Gln Leu Asn	Arg Leu	
302	1040	1045	1050		
304	gag acc cgg ctg agt	gca gac atg	gcc act gtc	ctg cag ctc	3384
305	Glu Thr Arg Leu Ser Ala Asp	Met Ala Thr Val	Leu Gln Leu	Leu Leu	
306	1055	1060	1065		
308	cag agg cag atg acg	ctg gtc ccg	ccc gcc tac agt	gct gtg acc	3429
309	Gln Arg Gln Met Thr Leu Val	Pro Pro Ala Tyr	Ser Ala Val	Thr	
310	1070	1075	1080		
312	acc ccg ggg cct	ggc ccc act	tcc aca tcc	ccg ctg ttg	3474
313	Thr Pro Gly Pro Gly Pro Thr	Ser Ser Pro	Leu Leu	Pro Val	
314	1085	1090	1095		
316	agc ccc ctc ccc acc	ctc acc ttg	gac tcg ctt tct	cag gtt tcc	3519
317	Ser Pro Leu Pro Thr Leu Thr	Leu Asp Ser	Leu Ser Gln	Val Ser	
318	1100	1105	1110		
320	cag ttc atg gcg tgt	gag gag ctg	ccc ccg ggg	gcc cca gag ctt	3564
321	Gln Phe Met Ala Cys	Glu Glu Leu	Pro Pro Gly	Ala Pro Glu Leu	
322	1115	1120	1125		
324	ccc caa gaa ggc ccc	aca cga cgc	ctc tcc cta	ccg ggc cag ctg	3609
325	Pro Gln Glu Gly Pro Thr Arg	Arg Leu Ser	Leu Pro Gly	Gln Leu	
326	1130	1135	1140		

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12

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